

FIGURE 1

GGACTAATCTGTGGGAGCAGTTTATTCCAGTATCACCCAGGGTGCAGCCACACCAGGACTGT
 GTTGAAGGGGTGTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTTCTTCTTACACAGTG
 TCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATAAATTCTACTTTTAGGAGGA
 CTACTCTCTTCTGCAGTCTTAGACTGGTCTTCTACACTAAGACACCATGAAGGAGTATGTG
 CTCCTATTATTCCTGGCTTTGTGCTCTGCCAAACCTTCTTTAGCCCTTACACATCGCACT
 GAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATGATGATGATGATG
 ATGATGATGATGAGGACAACCTCTCTTTTCCAACAGAGAGCCAGAAGCCATTTTTTCCA
 TTTGATCTGTTTCCAATGTGTCCATTGGATGTGCTAGTGCTATTACAGAGTTGTACATTGCTC
 AGATTTTAGGTTTGACCTCAGTCCCAACCAACATTCCATTGATACTCGAATGCTTGTATCTTC
 AAAACAATAAAATTAAGGAAATCAAAGAAATGATTTTAAAGGACTCACTTCACTTTATGGT
 CTGATCTCTGAACAACAACAGCTTAACGAAGATTACCCAAAAGCCTTTCTAACCCAAAAGAA
 GTTGCGAAGGCTGTATCTGTCCCACAATCAACTAAGTGAATACCACTTAATCTTCCCAAT
 CATTAGCAGAACTCAGAAATTCATGAAAATAAAGTTAAGAAAAATACAAAAGGACACATTCAAA
 GGAATGAATGCTTTACACGTTTTGGAAATGAGTGCAAAACCTCTTGATAATATGGGATAGA
 GCCAGGGGCAATTGAAGGGGTGACGGTGTTCATATCAGAATTCGAGAAGCAAAACTGACCT
 CAGTCTCTAAAGGCTTACCACCAACTTTATTGGAGCTTCACTTAGATTATAATAAAATTTTCA
 ACAGTGGAACTTGAGGATTTTAAACGATACAAAGAACTCAAAGGCTGGGCCTAGGAAACAA
 CAAAATCACAGATATCGAAAATGGGAGTCTTGCTAACATACCACGTGTGAGAGAAATACATT
 TGGAAAACAATAAACTAAAAAAAATCCCTTCAGGATTACCAGAGTTGAAATACCTCCAGATA
 ATCTTCTTCACTTAATTCAAATGCAAGAGTGGGAGTAAATGACTTCTGTCCAACAGTGCC
 AAAAGATGAAGAAATCTTTATACAGTGAATAGTTTATTCAACAACCCGGTGAATACTGGG
 AATGCAACCTGCAACATTTCTGTGTGTTTTGAGCAGAATGAGTGTTCAGCTTGGGAACTTT
 GGAATGTAATAATTAGTAATTGGTAATGTCCATTTAATATAAGATTCAAAAATCCCTACATT
 TGGAAATACCTTGAACCTATTAATAATGGTAGTATTATATATACAAGCAAAATATCTATTCTCA
 AGTGGTAAGTCCACTGACCTTATTTTATGACAAGAAATTTCAACGGAATTTTGCCAAACTATT
 GATACATAAGGGGTTGAGAGAAACAAGCATCTATTGCAGTTTCTTTTTGCGGTACAAATGAT
 CTTACATAAATCTCATGCTTGACCATTCCTTTCTTCATAACAAAAAAGTAAGATATTCGTA
 TTTAACACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTAATGGAATGCTTGACT
 TAGCAAAATTTGTCTCTTTTCATTGCTGTTAGAAAAACAGAATTAAACAAAGACAGTAATGT
 GAAGAGTGCATTACACTATTCTTATTCTTTAGTAACCTGGGTAGTACTGTAATATTTTAAAT
 CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTACCTTATCATGTCTTAGAGCCGT
 CTTTATGTTTAAAACTAAATTTCTTAAATAAAGCCTTCAGTAAATGTTCAATTACCACTTGA
 TAAATGCTACTCATAAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTTAAATTATT
 ACCTGATTTAAAAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAACCTCCGATTTT
 AATGATCCGCTATTATAAGCTTTTAATAGCATGAAATTTGTTAGGCTATATAACATTGCCAC
 TTAACCTTAAGGAATATTTTGAGATATCCCTTTGGAAGACCTTGCTTGGAAAGAGCCTGGGA
 CACTAACCAATTTACACCAAATGTCTCTTCAAAATACGTATGGAAGCTGGATAACTCTGAGAAA
 CACATCTAGTATAACTGAATAAGCAGAGCATCAAATTAACAGACAGAAACCGAAAGCTCTA
 TATAAATGCTCAGAGTCTTTTATGATTTCTTATTGGCATTCAACATATGTAAAAATCAGAAA
 ACAGGGAATTTTCATTAAAAATATTGGTTTGAAAT

FIGURE 2

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34392

<subunit 1 of 1, 379 aa, 1 stop

<MW: 43302, pI: 7.30, NX(S/T): 1

MKEYVLLLFALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDNSLFP TREPR
SHFFPFDLFP MCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKI KEIKENDFKGL
TSLYGLILNNNKLTKIHPKAFLTTKKLRLLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ
KDTFGGMNALHVLEMSANPLDNNGIEPGA FEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNK ITDIENGLANIPRVREIHLENNKLKKIPSGLP EL
KYLQIIFLHSNSIARVGVNDFCPTVPMKKS LYS AISLFNNPVKYWEMQPATFRCVLSRMSV
QLGNFGM

Signal sequence.

amino acids 1-15

N-glycosylation site.

amino acids 281-285

N-myristoylation sites.

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

Leucine zipper pattern.

amino acids 154-176
























CGACCGCTGGGGCGACGCGTGGGCGCGCGCGACGCCGCCCGCGCGCGCTCCGCCCTCGGCATCTCGGCGCTTCC
CTTCCCTCGCGCGCGCTCCGCGCGCTCTCTCTCTCTCTCTCCCGACGATGTCCGGTTTCGGGCTATGCGGACGATCC
GGCCCCCGCGCGCCCCGCTGTCTCTCTCGGGCTGCTGTCTGTCTCGGCTCCCGGCGCGCCCCGCGCGCGCGGCCAGA
GCCGCCCGCTGTCTGCCATCCGTTCTTGAGAAAGGACCGCTCGCCGTTCTGGGAGAGCGGAGAGCTGCACCTTCGGCGG
GAAGGTTCTATGCTTTGGAGGAGACGTGGCACCGACCTAGGACGACCAATCTCGGCGTGATGTCTGTCTGTCTGTG
CGCTCTCGGAGGCGCGCTCAGTGGGGTGGCGCTACGACAGGCGGCGCTTGGAGAGGCTCAGCTGCAGAAGACATCAACACAGA
TGCCCAACCCCGCGCTGTGTGGGACGACGCGACCTGTCCGGACAGACTGTCTCGAGACCTGCCCGAGAGCGACGAC
CAGTTTCGGAGCGGCGAGCGAGCGGCTGTCTCTTCAGATATCCGCGGGACCCGGAGACTCCGACCTTATATAGCGACG
CGGGAGCGACCGGCTGTAGGAGCGGGCCGCTGTGTGACGGGCCACCGGACTTCGTGGCGCTGCTGACGAGGCGGAG
GTGCGAGGCGGTGGACGAGGCGAGCTCGCTGTCTGTCTGTCTAGCTCCGCTCTCTATTCTTACAGCGCGCT
GGACGCGCCCTACAGATACCGTCTCTCAGACTCAATGGGCGAGTGTCTGTTTGAAGCACCTCGACGCCCCACCA
ATGATGCGTGTGTCTGTGGGTTGTGGCGGAGTGCCTCGTTGTCTGTCTGTCTTGGGCGCTTAGGGGACGAACAGTCA
TGTGGACCTTTGTACATCTACTACCTTCAGGGAGAGTGTGGGGGCTCTCATCCGACACCGGGCGCTTGCTGTG
AGAGACCTTCAGTCCCATCTGACTCTAGAAGGCCCCACGACGAGGCGTAGGGGCGACTACCCCTGTCTACTCT
CAGTGCACACAGAGACTCTTGATTTTTTGTGCTCTTCGAGGGCTCTGTGAACCCGAGATGGGGGAGCTAAC
CCAGGTTTCCTTTAGGCTCCAGATTTATACACGAGGGGAGCTACTCGAGAACTTCAGGCGCAATGTTCTCAGGCCA
GGAACAGGCTTTGTCTAGGTTGTGCCACACTGTACGTCAGGAGATGGACTGTGTCTGTGGGAGAGCTGCA
GATGGCGCTTGAGTGGGACGAGCGACGGGCTGCGCATCAGTGGACACTGTCTCGGAGGAAGAGTGTGCGAGT
CTCGAAAGTGTCTTTTTGGGGGCTGTATGCCCTGTACCTCCAGTACAGGGGTGTCTGCGCGCTCAGCCAGCTCAC
GCTGCTAGGAAATGGCTCCTGTATCTATCAGGTGCAAGTGTGATGGGACAAAGCAGTGAAGTGGTGCCCATGTACAT
GGAGACCAAGCTCAGCGGAGGATACGCGCATGTCTCGTCCATAGCTGCGACTCAGCGAGGAGGAGACAC
GCGCGTGGGTATGTCCCTGTGGCGTGGGTGGCCGAGGGGCTCATATGCTGTGTCAGATAGACTTTCTCTGAAGCT
GGCACCAAGAGCTTTCCAGAGCGAGAGCTTTGGGGGACAGTGGTGTCCCTGCTACTCTGTGGCATGTGCCCGC
CCATGACAGCTGCGCGTGCCCTGACGAGAGCGCTGTGTGTTACCCCTGTGGAAGAGCAAGCAGCGGCGACG
CTGGCTTTCTTGGATACCCATGTACCTGCATATGAAGTGTCTGTGCTGGCTGTGTGTGCTACGACAAAG
CATCTGCATCGCCACTCTTTGGGCTCTGTGAAGCCGCGGGCTCGCGCGCTGTGGAAGGGATTCTATGGCTC
AGAGGCGCAGGTTGTGTGAAGGACTGTGAGCGGAATCTGTGCGCACTGCGGCAAGAGGATGGCTCCTGTAT
GATCCACCAAGGAGGTAGCCCGACAGGAGGAGCTCGAGGCGAGTGCACATAGCCCAATGTAGTGTGGCGG
ACTCGGCTGTGAGGCGCGCGGGCGAGGGGGTGGGGGCTCGGGGCTTCGGATACAGCTGTGTGTGCGCGCC
TTGTGTGCTGTCTCCGCGCTACGCGCGCCCAATCTGTGGTCTTGGGCGCGCGAGACCCCAACATCAT
CTTCTTCAGGGGCGGACGCGCCCCACGGGCTCGCTGGGCGGCAATACAGCCCGCTCTGCTCATCTGCAC
CTGCGAGAGACGACGCTGTCTGTGACCGGGTGTGTGGCCACCGCCAGCTGCCCAACCCGGTGTGAGGCTCC
CGACAGTGCTGCCCTGTTCCTCTGAGAAACAGATATGTACAGACTTGCAGAGGCTGCGAAGGCGGGAGCC
AGAGAGGGCTGTATTATTGTGTGTCGAGCTGTGGCGGCGAGCGGTTACGCGGTGGCACCCGTTGTGCCCC
CTTTGGCTTTAATTAAGTGTCTGTCTGCACGTCAAGGGGGGACCTGTAGAGGGTGTGCACTGTGGAAGGTTGCA
TCCCGGCTGTGCTGTCTGCGGACGCTGTGCGTGTGTCAGCCAGCTGTCTGCAAAAGTGTCCAGTGGGTTGGG
GGCCCCCCCCAGCTGGGGGACCCATGCGAGCTGATGGGCGCTGGGGCTGCTTTTGTGTGGGCAGTGTTC
AGAGATGTACAGCTGTGCGACCCCTCAGTGGCCCCCTTTGGAGAGATAGCTGTCTGCGCTGCAGATGTGGGGGAG
GGTGTCTACTGTGTGAGCGGAGTGACTGTCTACTGCACTGTCTGTGTGGTGTGGGAGGAGATCGATGCTGTTC
CGGTCGACGCGGCGCCCGCGGCGGCGGACGACGACTGATCCAGAGCTGGAGAAAGGACGCAAGGCTCTTT
GGAGACGACGAGGGGCAAGTGACCAAGAGATGGGGCTGTGAGCTGGGAAGAGGTTGTCATCGAGGACTCTAT
GCATTTCTCTGTGGGAGCCGATGCTCTTTGCTCTCTGTCTGTCTACTTCCACCCCACTACTCTGGGAA
CCACAGCTCCCAAGGGGGAGAGGCGAGTGGGCGACCGAGGTGACAGCCACTCAAGTCTGCTCTGCCCTGCCACC
TCGGCTCTGTCTTGAAGAGCCACCCCTTTCTCTGTACATTAATGTCACTGCTGTGTGGGATTTTAAATTTA
TCTCTCAGCTCAGCACAGGGGCCCGGACATCACTCTCTGCTGCCCTGAGCTGAGCAGAGTCAATTATTTGAGAG
TTTTGTATTATTAAACATTTCTTTTCAGTCAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 4

><subunit 1 of 1, 954 aa, 1 stop

><MW: 101960, pI: 8.21, NX(S/T): 5

MPSLPAPPAPLLLLLGLLLLSRPARAGAGPEPPVLPISRSEKEPLPVRGAAGCTFGGKVYALDE
TWHPDLGQPPFGVMRCVLCACEAPQWGRRTRGPRVSCKNIKPECPTPACGQPRQLPGHCCQT
CPQERSSSSERQPSGLSFEYPRDPEHRYSYSDRGEPAEERARGDHTDFVALLTGPRSQAVAR
ARVSLRSSLRFSISYRRLLDRPTRIRFSDSNGSVLFEHPAAPTQDGLVCGVWRAVPRLSLRL
LRAEQLHVALVTLLTHPSGEVWGPLIRHRALAAETFSAILTLEGPPQQGVGGITLLTSLDTE
SLHFLLLFRGLLEPRSGGLTQVPLRLQILHQGLLRELQANVSAQEPGFAEVLPLNTVQEMD
WLVLGELQMALEWAGRPGLRISGHIAARKSCDVLSVLCGADALIPVQTGAAGSASLTLLGN
GSLIYQVQVVGTSSEVVAMTLETKPQRDRQRTVLCHMAGLQPGGHTAVGICPGLGARGAHML
LQNELFLNVGTDKDFPDGELRGHVAALPYCGHSARHDTLPVPLAGALVLPVKSQAAGHAWLS
LDTHCHLHYEVLLAGLGSGEQGTVAHLLGPPGTPGPRRLKGFYGSQAQGVVKDLEPELLR
HLAKGMASLMITTKGSPRGELRGQVHIANQCEVGGLRLEAAGAEGVRALGAPDTASAAPV
PGLPALAPAKPGGPRPRDPNTCFEFGQQRPHGARWAPNYDPLCSLCTCQRRTVICDPVVCP
PPSCPHVPQADPDCCPVCEKQDVRDLPGPLPRSRDPGEGCYFDGDRSWRAAGTRWHPVVPFF
GLIKCAVCTCKGGTGEVHCEKVQCPRLACAQPVVRNPTDCCCKCPVGSAGHPQLGDPMQADG
PRGCRFAGQWFPFESQSWHPSVPPFEGEMSCITCRCGAGVPHCERDDCSLPLSCGSGKESRCCS
RCTAHRPPPTRTDPELEKEAEGS

Signal sequence.

amino acids 1-23

N-glycosylation sites.

amino acids 217-221, 351-355, 365-369, 434-438

Tyrosine kinase phosphorylation sites.

amino acids 145-153, 778-786

N-myristoylation sites.

amino acids 20-26, 47-53, 50-56, 69-75, 73-79, 232-238, 236-242,
390-396, 422-428, 473-479, 477-483, 483-489, 489-495, 573-579,
576-582, 580-586, 635-641, 670-676, 773-779, 807-813, 871-877,
905-911

Amidation site.

amino acids 87-91

Cell attachment sequence.

amino acids 165-168

Leucine zipper pattern.

amino acids 315-337

FIGURE 5

GGCGGAGCAGCCCTAGCGCCACCGTCGCTCTCGCAGCTCTCGTCGCCACTGCCACCGCGCCGCCGCTCACTGCG
 TCCTGGCTCCGCTCCCGCGCCCTCCCGCGCGCCATGCGAGCCCCGCGCCAGGCGCCGGTGCAGCAGTGC
 TGCCCGGCTGCGCCCTGCTGCTGCTGCTGCTGCTGCGGAGCGGGGCCCCGAGGCGAGCTCCCTGGCCAAACCCGGTCCCG
 CCGCGCCCTTGTCTGCGCGCGGGCGCTGCGCGCGCAGCCCTGCGGAAATGGGGTGTGTGCACTTCGCGCCCTG
 AGCGGACCCGCGAGCACCCGCGCCCCGCGCGCGAGCTCGGTACAGCTGCACCTGCCCGCGGGATCTCCGGCG
 CCAACTGCCAGCTTGTTCAGATCCTTGTGCCAGAACCTTGTACCATTGGCAACTGCAGCAGCAGCAGCAGCA
 GCAGCAGCGATGGCTACCTCTGCATTGTCAATGAAGGCTATGAAGTCCCAACTGTGAACAGGCACTTCCAGTGC
 TCCCGAGCACTGGCTGGACCGAATTCATGGCACCCCGCAGCAGCTTCAGCCTGTTCTCTGCTACTCAGGAGCCTTGACA
 AAATCTGCTGCTGCTCAGGCAACGGTGACACTGCTACCTGGCAGCGAAAAACAGGCGAGAAAGTTGTAGAAA
 TGAATGGGATCAAGTGGAGGTATCCAGATATTGCTGTGGGAATGCCAGTTCTAACAGCTCTCGCGGTGGCC
 GCCTGGTATCCTTTGAAGTGCCACAGAACCTCAGTCAAGATTGCGCAAGATGCCACTGCCTCACTGATTGTTGC
 TCTGGAAGGTCACGGCCACAGGATTCCAAACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCCCTTCAGGCTT
 CAGGGGAGCTGGTCTCTCTGGAGGAGATGCTCGCCTTGGGGAATAATCACTTTATTGGTTTTGTGAATGATTCTG
 TGACTAAGTCTATTGTGGCTTTGCGCTTAACTCTGGTGGTGAAGGTGACACCTGTGTGCCGGGGAGAGTCAGC
 CAAATGCTTGGAGTGTTCAGGAAAGGAAATGCACACGAAAGCCGTCAGAGGCACTTTTCTGTCAGCTGTG
 AGGAGCAGTACGTGGGTATTTCTGTGAAGAATAAGATGCTTGGCAGAGGAATCTGCCAAACCAACGCGAGCTGT
 GTATTGATGCAAAATGAAAGCAAGATGGGAGCAATTTCACTGTGTTTGCCCTCTCGGTTATACTGGAGAGCTTT
 GCCAGTCCAAGATTGATTACTGCATCTAGACCCATGCGAGAAATGGAGCAACATGCATTTCAGCTCTCAGTGGAT
 TCACCTGCCAGTGTCCAGAAGGATACTTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCGCTCGCTCTCCGT
 GCCAGAACACCGCACCTGCTATGTGGACGGGTGACACTTTACCTGCACTGCAGCCCGGGCTTCACAGGGCCGA
 CCTGTGCCAGCTTATTGACTTCTGTGCCCTCAGCCCTGTGCTCATGGCAGTGCCGCGAGCTGGGCAACGAGCT
 ACAAAATGCCCTGTGTGATCCAGGTTACCATGGCTCTACTGTGAGGAGGAATATAATGAGTGCCTCTCCGCTCCAT
 GCCTGAATGCAGCCACTGCAGGGACCTCGTTAATGGCTATGAGTGTGTGCTGCCGAGAAATACAAAGGAACAC
 ACTGTGAATTGTACAAGGATCTCGCTAACGTCAGCTGTCTGAACGGAGCCACTGTGACAGCAGCGGCTGGA
 ATGGCAGCTGCATCTGTGCACCCGGGTTTACAGGTGAAGAGTGCAGCATTGACATAAATGAATGTGACAGTAACC
 CCTGCCACCATGGTGGGAGCTGCCGTGGACAGCCCAATGGTTATAACTGCCACTCCCGCAGTGGTTGGGTGGGAG
 CAAACTGTGAGATGCACCTCCAATGGAAGTCCGGGCACATGGCGGAGAGCCTCACCAACATGCCAGCGCATCCCT
 TCTACATCACTATTGGAGCCCTCTGCGTGGCTTCACTCTTATGCTGATCATCTGATCGTGGGGATTGCGGCA
 TCAGCCGATTGAATACCAGGGTTCTTCAGGCCAGCCCTATGAGGAGTTTACAACTGCCGAGCATCGACAGCG
 AGTTGACGAATGCCATTGCATCTCATCCGCAATGCCAGGTTTGAAGAAAGAAATCCCGGCTCGCAATGTATGATGTGA
 GCGTCATCGCTATGAAGATTACAGTCCCTGATGACAAACCTTGGTGCACATTAATAAACTAAAGATTGTAAT
 CTTTTTTTGGATTATTTTTCAAAAAGATGAGATACTACACTCAITTAATATTTTTTAAGAAAAATAAAGAGCTTAA
 GAAATTTAAATGCTAGCTGCTCAAGAGTTTTAGTAGAATATTTAAGAACAATTTTTCTGACGCTTTTATGTTTG
 GAAAAAATATTTTTAAAAACAAATTTTGTGAACCTATAGACGATGTTTTAATGTACCTTCAGCTCTCTAAACTGT
 GTGCTTCTACTAGTGTGTGCTCTTTTCACTGTAGACACTATCAGGAGACCCAGATTAAATTTCTGTGGTGTGTACA
 GATTAAGTCTAATCAAGGAGAGGTTTCTGTTTGAAGTTCAGGCGGCTTCTGAGTAGGTTAGGAAACCAAC
 GTAACTGATGATATGATGATATAAGATGATACCCGTTACTTAAAAAGAGTCTGAAGATGTTGCTTTTGTGGAAA
 AGAACTAGTATAAATTTACTATTCTTAACCCGAATGAATATAGCCTTTGCCCTTATTCTGTGCATGGGTAAAGTAAC
 TTATTTCTGCACGTGTTTGTGTAACCTTTGTGAAACATCTTCTGAGTTGTTTGTGTCATTGTTCTGAACAGCTG
 TCGAATAGGCCCTCAAAAACATACGTAAACGAAAGGCCCTAGCGAGGCAATCTGATTGATTGGAATCTATATT
 TTTCTTAAAAAGTCAAGGGTCTATATTGTGAGTAAATTAAGTTTACATTGAGTGTGTTGTTGCTAAGAGGTAG
 TAAATGTAAAGAGTACTGGTTCCTCAGTAGTGAGTATTCTCATAGTGACGCTTTATTATCTCCAGGATGTT
 TTTGGCGTGTATTGATTGATATGTGCTTCTCTGATCTTGCTAATTTCCAACCATATTGAATAAATGTGATC
 AAGTCA

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLPALALLLLLGAGPRGSSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR
PEPDPQHPAPAGEPGYSTCPAGISGANQQLVADPCASNPCHHGNCSSSSSSSDGYLCICN
EGYEGNCEQALPSLPATGWTESMAPRQLQPVPAQEPDKILPRSQATVTLPTWQPKTGQKV
VEMKWDQVEVIPDIACGNASSNSSAGRLVSEFVQNTSVKIRQDATASLILLWKVTATGFQ
QCSLIDGRSVTPLQASGGVLVLEEMLAGNNHFIGFVNDVSVTKSIVALRLTLVVKVSTCVPG
ESHANDLECSGKGKCTTKPSEATFSCTEEQYVGTFC EEYDACQRKPCQNNASCIDANEKQD
GSNFTCVCLPGYTGELCQSKIDYCILDFCRNGATCISSLSGFTCQCEPGYFGSACEEKVDPC
ASSPCQNNGTCTYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSYKCLCDPG
YHGLYCEEEYNECLSAFCLNAAATCRDLVNGYECVCLA EYKGT HCELYKDP CANVSC L NGATC
DSDGLNGTCTICAPGFTGEECDIDINECDSPCHHGSGCLDQPNGYNCHCPHG WVGANCEIHL
QWKS GHMAESLTNMPRHSLYIIIGALCVAFILMLIILIVGICRISR IEYQGSSRPAYEEFY N
CRSIDSEFSNAIASIRHARFGKKS RPAMYDVSP IAYEDYSPDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

FIGURE 7

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTCAGGCCTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTT
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTTCCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTTGCCTTCC
TGTTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

1000
900
800
700
600
500
400
300
200
100
0
1000
900
800
700
600
500
400
300
200
100
0

FIGURE 8

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCTTTTCAGGCTTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTC
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC
TGTTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

1000
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500
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300
200
100
0
1000
900
800
700
600
500
400
300
200
100
0

FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCCAGCCTGTAACCTGTGCCTACACCACGCCAG
GCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCAGAGCCACACCATGCGGGGCACCTAC
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT
GATGCGGGACTTCCCCTCGTGGACGGCCACAACGACCTGCCCTCGGTCTTAAGGCAGTTT
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTTCAGCTACGGCCAGACCAGCCTGGAC
AGGCTTAGAGATGGCCTCGTGGGCGCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATACGCCGATGTGTGCCCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
CTACATGCTGGGAGTGCCTACCTGACGCTCACCCACACCTGCAACACACCTGGGCAGAGA
GCTCCGCTAAGGGCTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG
AAGTGTTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGTGCC
GGGTGTGTGCAACAGTGTCTCGAATGTTCTTGATGACATCCTGCAGCTTCTGAAGAAGAAC
GGTGGCGTGTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGT
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCAATTGGATCCAAGTTTCATCGGGA
TTGGTGGAGATTATGATGGGGCCGGCAAATTCCTCAGGGCTGGAAGACGTGTCCACATAC
CCGGTCTGATAGAGAGTTGCTGAGTGTGCTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTT
TCGTGGAAACCTGCTGCGGGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAAAAATGGC
AAAGCCCCCTGGAGGACAAGTTCCTGGATGAGCAGCTGAGCAGTTCTTGCCACTCCGACCTC
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACTCACTGAGATTCCCATACA
CTGGACAGCCAAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCTCCCCCACATGGCCCCAG
TCCTTGCACTTGTGGCCACCTTCCCAGTCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCTCTGTGTGCAGGCACA
AATATTTCTGAAATAAATGTTTGGACATAG

FIGURE 10

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA35595

<subunit 1 of 1, 433 aa, 1 stop

<MW: 47787, pI: 6.11, NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQRALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILO
LLKKNGGVVMVSLSMGVIQCNP SANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHMAPVLAVVATFPVLILWL

N-glycosylation sites.

amino acids 58-62, 123-127, 182-186, 273-277

N-myristoylation sites.

amino acids 72-78, 133-139, 234-240, 264-270, 334-340, 389-395

Renal dipeptidase active site.

amino acids 134-157

FIGURE 11

AAAACTATAAATATTCCGGATTATTATACACCGTCCACCATCGGGCGCGGATCCGCGGCCG
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA
CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCCCTCGTGGACGGCCAC
AACGACCTGCCCCCTGGTCTTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTTAACCTGCG
CAATTTCAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCAGT
TCTGGTCAGCCTATGTGCCATGCCAGACCAGGACCGGGATGCCCTGCGCCTCACCTGGAG
GAGATTGACCTCATACGCCGATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCCTACCTGACGCTC
ACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGTGGTGGCAGAAATGAACCGCTGGGCA
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTACAG
GCACCTGTGATCTTCTCCCACTCGGCTGCCCCGGGTGTGTGCAACAGTGTCTCGGAATGTTCC
TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTGTGATGGTGTCTTTGTCCATGG
GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC
AAGGCTGTCAATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT
CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCTGATAGAGGAGTTGCTGAGTCTGTG
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCTGCGGAAACCTGCTGCGGGTCTTCAGACAA
GTGGAAGAGGTACAGGAAGAAAAAAATGGCAAAGCCCCTTGGAGGACAAGTTCCCGGATGA
GCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCAGTCTGCGTCAGAGACAGAGTCTGACTT
CAGGCCAGGAACCTCACTGAGATTCCCATACACTGGACAGCCAAGTTACCAGCCAAGTGGTCA
GTCTCAGAGTCTCCCCCACCTGACAAAACCTCACATGCCACCGTGGCCAGCACCTGA
ACTCTGGGGGACCGTCAGTCTTCTCTTCCCCCAAAACCAAGGACAC

FIGURE 12

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MPGTYPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNNGVVMVSLSMGVIQCNPSPANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPLVIEELLSRGWSEBELQGVLRGNLLRVFRQVEKVQEEKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHDPKTHTCPPCPAPELLGGP
SVFLFPPKPKDT
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[illegible]

CGCCACAGCGACGTGCGGGCGGCCTGGCCGCGCCCTCCGCGCCCCGGCCTGCTCCCGCGCC
CTGCGCCACCGCCGCGGAGCCGAGCCCGCGCGCGCCCCCGGCAGCGCCGGCCCC**CATG**CCC
GCCGGCCGCGGGGGCCCCGCGCCCAATCCGCGCGCGCGCCCGCCGCTTGCTGCCCCCTGCT
GCTGCTGCTCTGCGTCTCTCGGGGCGCCGCGAGCCGATCAGGAGCCACACAGCTGTGATCA
GTCCCCAGGATCCACAGCTTCTCATCGGCTCCTCCTGCTGGCCACCTGCTCAGTGACGGGA
GACCCACACAGGAGCCACCGCGGAGGGCCTTACTGGACCCTCAACGGGCGCCGCTGCCCCC
TGAGCTCTCCCGTGTA**CTCA**ACGCCCTCCACCTTGCGCTCTGGCCCTGGCCAACCTCAATGGGT
CCAGGCAGCGGTGCGGGGACAACCTCGTGTGCCACGCCCGTGACGGCAGCATCCTGGCTGGC
TCCTGCTCTATGTTGGCCTGCCCCAGAGAAACCCGTCAACATCAGCTGCTGGTCCAAGAA
CATGAAGGACTTGACCTGCCGCTGGACGCCAGGGGCCACCGGGAGACCTTCTCCACACCA
ACTACTCCTCAAGTACAAGCTTAGTGGTATGGCCAGGACAACATCATGTGAGGAGATACCAC
ACAGTGGGGCCCACTCTGCCACATCCCAAGAGCACTGGCTCTCTTTACGCCCTATGAGAT
CTGGGTGGAGGCGACCAACCGCTGGGCTCTGCCCGCTCCGATGTACTCAGCTGGATGATCC
TGGAATGTGTGTACCACGGACCCCGCGCGACGTGCACGTGAGCCGCGTGGGGGCTGGAG
GACCAGCTGAGCGTGCCTGGGTGTGCGCACCCGCCCTCAAGGATTTCTCTTTCAAGCCAA
ATACAGATCCGCTACCGAGTGGAGACAGTGTGGA**CTG**GAAGGTGGTGGACGATGTGAGCA
ACCAGACCTCCTGCCGCTGGCCGGCCTGAAACCGGCACCGTGTA**CTT**CGTGCAAGTGCGC
TGCAACCCCTTTGGCATCTATGGCTCCAAGAAAGCGGGATCTGGAGTGAGTGGAGCCACCC
CACAGCCGCTC**CACT**CCCCGAGTGAGCGCCCGGGCCCGGGCGCGGGGCGTGCGA**AC**CGC
GGGGCGGAGAGCCGAGCTCGGGGCGCGTGCGGCGCGAGCTCAAGCAGTTCTGGGCTGCGCTC
AAGAAGCAGCGTACTGCTCAACCTCAGCTTCCGCCTCTACGACCAAGTGGCGAGCCTGGAT
GCAGAAGTCGCACAAAGACCCGCAACAGGACGAGGGGATCCTGCCCTCGGGCGAGCGGGGCA
CGGCGAGAGGTCCTGCCAGAT**TAA**AGCTGTAGGGGCTCAGGCCACCTCCCTGCCACGTGGAGA
CGCAGAGGCCGAACCCAA**ACT**TGGGGCCACCTCTGTACCTCACTTACAGGGCACCTGAGCCAC
CCTCAGCAGGAGCTGGGGTGGCCCTTGAGCTCCAACGGCCATAACAGCTCTGACTCCACGT
GAGGCCACCTTTGGGTGCACCCAGTGGGTGTGTGTGTGTGTGTGAGGGTTGGTTGAGTTGC
CTAGAACCCTGCCAGGCTGGGGGTGAGAAGGGAGTACTTACCTCCCACTTACCTAGGGCC
CTCCAA**AAAG**AGCTCTTTTAAATAAATAGAGCTATTAGTGCTGTGATTTGTGA**AAAA**AAAAA
AAAAA
AAAAA

FIGURE 14

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSARRPPPLPLLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATCSV
HGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCSWSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEE
YHTVGPCHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSrvGG
LEDQLSVRWVSPPALKDFLFQAKYQIRYRVEDSVDWKVVDVSNQTSCLAGLKPGTVYFVQ
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSGSPVRRELKQFLG
WLKKHAYCSNLSFRLYDQRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

FIGURE 15

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTATTCTCTAA
GAGGAGAAAATCAGTCACCGCGGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCTATGAATTTGCTAAACTTAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTCATACCTTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTGTTTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA
GGCATTCTTCTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCTCTTACTGGCTTACTGTTCAAGCAAGTTTGTGCTGTTGGA
TTTCATAAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
TCTGTGCTCTAATTTTCGTAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCCTGAGCGTTT
CCTGGCAGTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTTTCTGAAAACGATTTACCAGGTTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTTAATGTTTGAACCTTCTGTTTTTCTAATTATCCCCATTTCTTCAATA
TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTTATTAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
AATTTGTACCATAACCGTTTATTAAACATATATTTTTATTTTTGATTGCACTTAAATTTGT
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAAACTTCAAGCTCTCTAATAAAAA
TGAAGGACTATATCTAGTGGTATTTCAATGAATATCATGAACTCTCAATGGGTAGGTTTC
ATCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCGAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGTGGATACAGTGTGCAAGTATAAAGCATCACTGGGATTTAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AA

FIGURE 16

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

MKFLLDILLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDSCNREDIYSSAKKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTASAAGHVSVFPLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 17

GA CTAGTTCTCTTGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTG
GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGAGAAGCGCGGGGGCTGGAGCACCACCAA
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT
GCAGAGGACCCCGCGTCCGGGCTCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCTCTGC
TGCTCTCTGGGCTGGCGGCCGCTCGCCCCACTGGACGACAACAAGATCCCAGCCTCTGC
CCGGGGCACC CGCCTTCCAGGCACGCCGGGCCACCATGGCAGCCAGGGCTTGCCGGGCCG
CGATGGCCGCGACGGCCGCGACGGCGCGCCCGGGGCTCCGGGAGAGAAAGCGAGGGCGGGA
GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGGGGG
CCCACCGGGCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC
CGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCCTGCCCCCTCGACCGCGTGCTGGTGAACG
AGCAGGGACATTACGACGCCGTACCGGCCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC
TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA
ATCCATTGCCTCTTTCTTCCAGTTTTTCGGGGGGTGCCCAAGCCAGCCTCGCTCTCGGGGG
GGGCCATGGTGAGGCTGAGCCTGAGGACCAAGTGTTGGTGAGGTGGGTGGGTGACTAC
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGATTCTGGTGTA CTCCGA
CTGGCACAGCTCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTCC
TAGAAGGAGGGTGTGAGGCTGACAACCAAGGTATCCAGGAGGGCTGGCCCCCTGGAATATT
GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCTGTGCTGGCAAGGAATGGGAAC
AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTCTGCCCAAGACCA
GAGGAGTGTGCTGTGCTGGCAAGTGTAAGTCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT
GGGGTGCTCTTCTCTGGTCTCTGCTTCTCTGGATCTCCCCACCCCTCTGTCTCTGGG
GCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCTCATAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAP
GEKGEGRPGPLPGPRGDPGRGEAGPAGPTGPAGECSVPPRSAFSKRSESRVPPPSDAPLP
FDRVLVNEQGHYDAVTGKFTCQVPGVYFVAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

FIGURE 19

CTCTTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCTGGCCCTCCTTG
GCACCACCTGGGCAGAGGTGTGGCCACCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTTCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCACTGGCTCAAG
CCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCTTG
CAAGTGGGCTGGAACATGCAGCTGCTGCCCCGCGGCTTGGCGTCCTTTGTTGAAGTGGTCAG
CCTATGTTTTCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGCTGCGCAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGCGGCAC
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCTACTCCCCGGAGGCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCTATAAGAAGGGTGCCCTGGTGTTCGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC
AGGAATCCTTGTGCGATGAGCTGCCAGAACCATGGACGCTCTCAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC
ACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGCGTCTGTGACATCGGCTACGGGGGAGCCAG
TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGCTTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTGAGAGGAAAGCG
GGGTGCTGGCCAGATCAAGAGCCAGAAAGTGACGACATCCTCGCCTTCTATCTGGGCCGC
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACCTTCTGGATCGGGCT
CACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACAGGCCCTTACCA
GTTTGTGCTTTGGGCAGCCTGACAAACCAGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAAC
CCGAAACCGTTACATCTGCCAGTTTGGCCAGGAGCACATCTCCCGTGGGGCCAGGGTCTT
GAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCCAGGTTAAGACCACATGCCTCATGTCCAAGAGGTCTCAGA
CCTTGCACAATGCCAGAAGTTGGGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAAGGCTGCTCTCTTCCACCTGGCCAGAC
CCTGTGGGGCAGCGAGCTTCCCTGTGGCATGAACCCACGGGTATTAATTTATGAATCAG
CTGAAAAAAAAAAAAA

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176
<subunit 1 of 1, 455 aa, 1 stop
<MW: 50478, pI: 8.44, NX(S/T): 2
MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEAPMAGALNRKESFLLLSLHNRLRSWV
QPPAADMRRLLDWSDSLALQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSSAGQTAIEAFVCAYSPPG
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSQCNHGRNLNISTCH
CHCFPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDC
FMVSSEADTYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLTTNEVTDSDFETRNFWIG
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWL SAAMGFGNCVELQASAAFNWDQRCK
TRNRYICQFAQEHISRWGP GS

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442

FIGURE 21

CGGACGCGTGGGCTGGGCGCTGCAAAGCGTGTCCGCGGGTCCCCGAGCGTCCCGCGCCCT
CGCCCCG**CATG**CTCCTGCTGCTGGGGCTGTGCCTGGGGCTGCCCTGTGTGTGGGGTCGCA
GGAAGAGGCGCAGAGCTGGGGCCACTCTCGGAGCAGGATGGACTCAGGGTCCCGAGGCAAG
TCAGACTGTTGCAGAGGCTGAAAACCAACCTTTGATGACAGAATTCTCAGTGAAGTCTACC
ATCATTTCGGTTATGCGCTTACTACGGTTTCCTGCAGAATGCTGAACAGAGCTTCTGAAGA
CCAGGACATTGAGTTCAGATGACAGATTCCAGCTGCAGCTTTTCATCACCAACTTCACTATGC
TTATTGGAGACAAGGTGTATCAGGGCGAAATTACAGAGAGAGAAAAGAGTGGTGATAGG
GTAAAGAGAAAAGGAATAAAACCACAGAAGAAAATGGAGAGAAGGGGACTGAAATATTAG
AGCTTCTGCAGTGATTCCAGCAGGACAAAGCGCGCTTTTCTCAGTTATGAGGAGCTTC
TGCAGAGGCGCCTGGGCAAGTACGAGCACAGCATCAGCGTGCAGGCCAGCAGCTGTCCGGG
AGGCTGAGCGTGGACGTGAATATCCTGGAGAGCGCGGCATCGCATCCCTGGAGGTGCTGCC
GCTTCACAACAGCAGGACAGAGGGGCACTGGGCGCGGGGAAGATGATTCTGGGCTCCCCAT
CTACTGTCAATAACCAAAATGAAACATTTGCCAACATAATTTTAAACCTACTGTAGTACAA
CAAGCCAGGATTGCCAGAAATGGAATTTTGGGAGACTTTATCATTAGATATGACGTCAATAG
AGAACAGAGCATTGGGGACATCCAGGTTCTAAATGGCTATTTTGTGCACTACTTTGTCTCCTA
AAGACCTTCTCTCTTACCAAGAATGTGGTATTCTGTGCTTGACAGCAGTGCTTCTATGGTG
GGAACCAAACTCCGGCAGACCAAGGATGCCCTCTTCACAATTCTCCATGACCTCCGACCCCA
GGACCGTTTCAGTATCATTGGATTTCACCAACGGATCAAAGTATGGAAGGACCACTTGATAT
CAGTCACTCCAGACAGCATCAGGGATGGGAAAGTGACATTACCATATGTACCCCACTGGA
GGCACAGACATCAACGGGGCCCTGCAGAGGGCCATCAGGCTCCTCAACAAGTACGTGGCCCA
CAGTGGCATTTGGAGACCGGAGCGTGTCCCTCATCGTCTCTCTGACGGATGGGAAGCCACGG
TCGGGGAGACGCACACCCTCAAGATCCTCAACAACCCGAGAGGCCGCCCGAGGCCAAGTC
TGCATCTTCAACATTGGCATCGGCAACGACGTGGACTTCAGGCTGTGGAGAACTGTCTCGT
GGAGAATGTGGCCTCACACGGCGCTGCACGAGGAGGAGGACGCGAGGCTCCGAGCTCATCG
GGTCTACGATGAAATCAGGACCCCGCTCCTCTCTGACATCCGCATCGATTATCCCCCAGC
TCAGTGTGCGAGGCCACCAAGACCTGTTCCCAACTACTTCAACGGCTCGGAGATCATCAT
TGCGGGGAAGCTGGTGGACAGGAAGCTGGATCACCTGCAGTGGAGGTACCGCCAGCAACA
GTAAGAAATTCATCATCCTGAAGACAGATGTGCCTGTGCGGCCCTCAAGAGGACGGGAAAGAT
GTACAGGAAGCCCCAGGCTGGAGGCGATGGAGAGGGGGACCAACCACATCGAGCGTCT
CTGGAGCTACCTCACCAAAAGGAGCTGCTGAGCTCCTGGCTGCAAAGTGACGATGAACCGG
AGAAGGAGCGGCTGCGGCAGCGGCCAGGCCCTGGCTGTGAGCTACCGCTTCTCACTCCC
TTCACCTCCATGAAGCTGAGGGGGCCGGTCCCACGCATGGATGGCTGGAGGAGGCCACGG
CATGTCCGCTGCCATGGGACCCGAACCGGTGGTGACAGCGTGCAGGAGCTGGCACGCGC
GAGCACTTTGCTCAAGAAGCCAACTCCGTCAAAAAAACAACCAAAAAAAGAA
CATGGGAGAGATGGTGTTTTCTCTCCACCACCTGGGGATACGAT**TGA**GAAGATGGCCACTT
GCAGGAGGAAGACGGCCCTCACAGACCATGTCTGTGACACCTTGATGTGACCTTGGACCT
CCAGCTCCAGAACTGTGAGAAATAAATGTGTTTTGTTTAAAGCTAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 22

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLLQRLKTKPLMTEFSVKSTIIIS
RYAFTTVSCRMLNRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKE
KRNKTEENGEKGTEIFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVSRPQQLSGRLS
VDVNILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPTVINQNETFANIIFKPTVVQAR
IAQNGILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFVLDSSASVMGK
LRQTKDALFTILHDLRPQDRFSIIGFSNRIKVKWDHLISVTPDSIRDGVYIHHMSPTGGTD
INGALQRAIRLLNKYVAHSGIGDRSVSLIVFLTGDGKPTVGETHTLKILNNTREAAARGQVCIF
TIGIGNDVDFRLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVV
QATKTLFPNYFNGSEII IAGKLVDKRLDHLHVEVTASNSKKFIILKTDVPRPQKAGKDVGTG
SPRPGDGEGDTHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTS
MKLRGPVPRMDGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKKQNKTKKRHGR
DGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

FIGURE 23

CGGACGCGTGCGGTGCCGACATGCGCAGTGTAGTGCTGCCGAGCGGATCCCACTGTGCGGC
GGCAGCGCGCGCGCGCGCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGG
CACTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGTGAGGGGA
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTACAGCTACTGAA
TCCCAACAGGCAGACCATTTATTTTACAGGACTTCAGGCCTTTGAAGGACAGCAGGTTTCAGT
TGCTGAATTTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTTCTGTATGAA
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCACAGGAAAGTTACACCACCATCACAGT
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAA
GGGAACACAGAGCTAAAAGGCAAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGTATCTGCCAGGTGG
AGCACCTTGGGTCACTGGAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGCACATTCAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGACGCGCTTGA
GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACCTGGGTGAGAGTCGATG
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCAACCTGTTTCATCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCACAACATATCCCTCCTCCCAACAACACCACCACCA
CCACCACCACCACCACCACCATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGC
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCTGGCGGTGGTGGTGTTCGCCAT
GCTGTGCTTGTCTCATATCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA
GGACAGAACAACCTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTTGTTCAT
GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGTATTTGG

FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pI: 4.93, NX(S/T): 7
MASVVLPSGSQCAAAAAAAPPGLRLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISC
QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSELKVSLTNVSIISDEGRYFCQL
YTDPPQESYTTITVLVPPRNLMDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG
KSEVEEWSDMYTVTSQLMLKVHKEDDGVFVICQVEHPAVTGNLQTQRYLEVQYKPVVHIQMT
YPLQGLTREGDALELTCEAIGKPQFVMVTWVRVDEMPQHAVLSGPNLFINNLNKTDNGTYR
CEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTILTIIITDSRAGEEGSIRAVDH
AVIGGVVAVVVFAMLCLLIILGRYFARHKGYTFTEAKGADDAADADTAIINAEGGQNNSEE
KKEYFI

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.

amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434

Tyrosine kinase phosphorylation sites.

amino acids 233-240, 319-328

N-myristoylation sites.

amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

FIGURE 25

GGGGCGGGTGGACGCGGACTCGAAACGCAAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCGA
 CCGGCCAGGAAAGACTGAGGCCGCGGGCTGCCCCGCCGGCTCCCTGCGCCGCGCGCGCTC
 CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT
 GGGGCCCTGGGGTGCAGGGCTGCCCATCCGGTGCCAGTGCAGCCAGCCACAGACAGTCTTCT
 GCACTGCCCGCCAGGGGACCAGGTGCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC
 GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCTGCGGGCCCTGCA
 GCTCCTGGACCTGTACAGAACCAGATCGCCAGCCTGCGCCTGCCCGCCTGCTGCTGCTGG
 ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAG
 GCCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGAACGAGGGCTCTTCAGCCGCTTGG
 CAACCTCCACGACCTGGATGTGTCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG
 GCCTCCGGGGCTGACGCGCTGCGGCTGGCCGGCAACACCCGATTGCCAGCTGCGGGCC
 GAGGACCTGGCCGGCTGGCTGCCCTGCAGGAGCTGGATGTAGCAACCTAAGCCTGCAAGC
 CTTGCTGGCGACCTCTCGGGCTCTTCCCCCGCTGCGGCTGCTGGCAGCTGCCCGCAACC
 CTTCAACTGCGTGTGCCCTGAGCTGGTTTGGCCCCGGGTGCGCGAGAGCCACGTACACA
 CTGGCCAGCCTTGAGGAGACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCT
 GGAGCTTTGACTACCGCACTTTGGCTGCCAGCCACCCACAGCAACGATGGCCGCTTACCA
 CGAGGCCCTGCTGCGGGAGCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGC
 CCCCACGCGCCGCCACTGAGGCCCCAGCCCGCCTCCACTGCCCCACCGACTGTAGGGCC
 TGTCCCCAGCCCCAGGACTGCCACCGTCCACTGCTCAATGGGGGCACATGCCACCTGG
 GGACACGGCACCACTGGCGTGTCTGTGCCCGAAGGCTTCACGGGCTGTACTGTGAGAGC
 CAGATGGGGCAGGGACACGGCCAGCCTACACAGTCAAGCCGAGGCCACCAAGGTCCCT
 GACCTGGGCGATCGAGCCGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCC
 AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
 AAGCGGCTGGTGACGCTGCGACTGCTGCTCGCTCGCTGAGTACACGCTCACCAGCTGCG
 GCGCAACGCCACTTACTCGCTGTGTCTATGCTTTTGGGGCCGGCGGGTGGCGGAGGGCG
 AGGAGGCTGCGGGGAGGCCCATACACCCAGCCGCTCCACTCCAACACGCCCCAGTCAAC
 CAGGCCCGCGAGGGCAACCTGCGCTCCCTCATTTGCGCCCGCCCTGGCCGCGGTGCTCCTGGC
 CGCGCTGGCTGCGGTGGGGGCGAGCTACTGTGTGCGGGCGGGGGCGGCCATGGCAGCAGCGG
 CTCAGGACAAAGGGCAGGTGGGGCCAGGGCTGGGCCCCGGAACCTGAGGGAGTGAAGGTC
 CCCTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGTCTGA
 GTGTGAGGTGCCACTCATGGCTTCCCAGGGCCTGGCTCCAGTCAACCCCTCCACGCAAAAGC
 CTTACCTAGGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAATGGC
 CAGCCCCCTCTGCTGCCACACCAGTAAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA
 CAGGGCTGTGTGACCAAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCTCATCTGTGAG
 ATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCGAACCAGTGCCTATGAGGACAGTGT
 CGGCCCTGCCCTCCGCAACGTGCACTCCCTGGGCACGGCGGGCCCTGCCATGTGCTGGTAAC
 GCATGCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCCTGGGGGCGAGTGAAGGAAG
 CTCCCGGAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTCTAGTCTTGGCCCCAGG
 AAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAACATGTTTTGCTTTTTTAA
 AATATATATATATTTATAAGAGATCCTTTCCTATTATTCTGGGAAGATGTTTTTCAAACTC
 AGAGACAAGGACTTTGGTTTTTGTAAAGCAACAGATGATATGAAGGCCTTTTGTAAAGAAAA
 ATAAAAAAAAAA

FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44804

<subunit 1 of 1, 598 aa, 1 stop

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVPLLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPVPRDVPDTPVGLYVFEN
GITMLDASSFAGLPGLQLLDLSQNIASRLRLPRLLLDLSHNSLLALEPGILDANVEALRL
AGLGLQQLDEGLFSRLRNLDLDVSDNQLERVFPVIRGLRGLTRLRLAGNTRIAQLRPEDLA
GLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFGPWVRESHVTLASP
EETRCHFFPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPTWLSPTAP
ATEAPSPPTAPPTVGVPVQPQDCPPSTCLNGGTCHLGRHHLACLCEGFTGLYCESQMGQ
GTRPSPTPVTPRPPSLTLGIEPVSPSLRVGLQRYLQGS SVQLRSLRLTYRNLSGPDKRLV
TLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE
GNLPLLIAPALAAVLLAALAAGVGAAYCVRGRAMAAAAQDKQGVGPGAGPLELEGVKVPLEP
GPKATEGGGEALPSGSECEVPLMGFPFGPLQSPHAKPYI

Signal sequence.

amino acids 1-23

Transmembrane domain.

amino acids 501-522

N-glycosylation sites.

amino acids 198-202, 425-429, 453-457

Tyrosine kinase phosphorylation site.

amino acids 262-270

N-myristoylation sites.

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

EGF-like domain cysteine pattern signature.

amino acids 355-367

Leucine zipper pattern.

amino acids 122-144, 194-216

FIGURE 27

GGCACTAGGACAACCTTCTTCCCTTCTGCACCACTGCCCGTACCCTTACCCGCCCCGCCACC
TCCTTGCTACCCCACTCTTGAAACCAAGCTGTTGGCAGGGTCCCCAGCTC**ATG**CCAGCCTC
ATCTCCTTTCTTGCTAGCCCCCAAAGGGCCTCCAGGCAACATGGGGGGCCAGTCAGAGAGC
CGGCACTCTCAGTTGCCCTCTGGTTGAGTTGGGGGGCAGCTCTGGGGGCCGTGGCTTGCGCC
ATGGCTCTGCTGACCCAAACAAACAGAGCTGCAGAGCCTCAGGAGAGAGGTGAGCCGGCTGCA
GGGGACAGGAGGCCCTCCAGAAATGGGGAAGGGTATCCCTGGCAGAGTCTCCCGAGCAGA
GTTCCGATGCCCTGGAAGCCTGGGAGAATGGGGAGAGATCCCGAAAAGGAGAGCAGTGCTC
ACCCAAAAACAGAAGAAGCAGCACTCTGTCTTGACCTGGTTCCCATTAACGCCACCTCCAA
GGATGACTCCGATGTGACAGAGGTGATGTGGCAACAGCTCTTAGGCGTGGGAGAGGCCTAC
AGGCCCAAGGATATGGTGTCGGAATCCAGGATGCTGGAGTTTATCTGCTGTATAGCCAGGTC
CTGTTTCAAGACGTGACTTTACCATGGGTCAGGTGGTGTCTCGAGAAGGCCAAGGAAGGCA
GGAGACTCTATTCCGATGTATAAGAAGTATGCCCTCCACCCGGACCGGGCTACAACAGCT
GCTATAGCGCAGGTGTCTTCCATTTACACCAAGGGGATATTCTGAGTGTCAATAATCCCCGG
GCAAGGGCGAAACTTAACCTCTCTCCACATGGAACCTTCTGGGGTTTGTGAAACT**TGAT**T
GTGTTATAAAAAGTGGCTCCAGCTTGGAAGACCAGGGTGGGTACATACTGGAGACAGCCAA
GAGCTGAGTATATAAAGGAGAGGGAATGTGCAGGAACAGAGGCATCTTCTGGGTTTGGCTC
CCCGTTCCTCACTTTTCCCTTTTCATTCCCACCCCTAGACTTTGATTTTACGGATATCTTG
CTTCTGTTCCCCATGGAGCTCCG

FIGURE 28

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52722

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27433, pI: 9.85, NX(S/T): 2

MPASSPFLLAPKGGPGNMGPPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV
SRLQGTGGPSQNGEGYPWQSLPEQSSDALEAWENGERSRKRRAVLTQKQKKQHSVLHLVPIN
ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVFTFMGQVVSREG
QGRQETLFCIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIIPARAKLNLSPHGTFGLGFVKL

Signal sequence.

amino acids 1-40

N-glycosylation site.

amino acids 124-128

Tyrosine kinase phosphorylation site.

amino acids 156-164

N-myristoylation site.

amino acids 36-42, 40-46, 179-185, 242-248

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 34-45

FIGURE 29

CACTTTCTCCCTCTCTTCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGTGTCGACAGAC
CTCGGAGACCGCGCCGGGAGACGGAGGTGCTGTGGGTGGGGGGACCTTGTGGCTGCTCGTA
CCGCCCCCACCCTCCTCTTCTGCACTGCCGTCTCCGGAAGACCTTTCCCTGCTCTGTT
TCCTTCACCGAGTCTGTGCACTCGCCCCGGAACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA
TGCTCTAGGGGGCGCGCGGGAGGAGCGGCCGGCGGACGGAGGGCCCGGAGGAAGATCGGC
TCCGTTGACAGGGACTCTTGTGGCGTACTGCCTGCTCTTGCCTTGGCTTCCCTGTGCTGCT
CCTGAGTCTGTGCCCCATGTCCAGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
CGTGCCTCCGAGACCATGCCGAGAGGGCTGAAGAACAACATGAAAAATACAGGCCCACTGAG
GACCAGGGGCTCCCTGCTTCCCGTGCTTGCCTGCTGTGACCCCGGTACCTCCATGTATACC
GGCGACCGCGTGTCCCGAGATCAACATCACTATCTTGAAAGGGGAGAAGGGGTGACCGCGAG
ATCGAGGCTCCAAGGGAATATGGCAAAACAGGCTCAGCAGGGGCCAGGGGCCACACTGGA
CCCAAAGGGCAGAAGGGCTCCATGGGGGCCCTGGGGAGCGGTGCAAGAGCCACTACGCCGC
CTTTTCGTTGGGCGGGAAGAGCCCATGCAACAGCAACCACTACTACGACCGGTGATCTTCG
ACACGGAGTTCTGTGAACCTCTACGACCACCTTCAACATGTTACCCGGCAAGTTCTACTGCTAC
GTGCCCCGCTCTACTTCTCAGCCTCAACGTGCACACCTGGAAACGAGAAGGAGACCTACCT
GCACATCATGAAGACGAGGAGGAGGTGGTGATCTTGTTCGCGCAGGTGGGCGACCGCAGCA
TCATGCAAGGCCAGAGCCTGATGCTGGAGTGCAGAGCAGGACCAGGTGTGGGTACGCCTC
TACAGGGCGAAGCTGAGAACGCCATCTTACGCGAGGAGCTGGAACACCTACATCACCTTCAG
TGGCTACCTGTCTCAAGCAGCCACCGAGCCCTAGCTGGCGGCCACCTCTTCTCTCTGCC
ACCTTCCACCCCTGCGCTGTGCTGACCCACCGCCTCTTCCCGCATCCTCGGACTCCGACTC
CCTGGCTTGTGGCATTGAGTGCAGCGCCCTGCACACAGAAAGCCAAAGCGATCGGTGCTCC
CAGATCCCGCAGCCTCTGGAGAGAGCTGACGGCAGATGAAATCACCAGGGCGGGGACCCCGC
GAGAACCTCTGGGACCTTCCGCGGCCCTCTTGCAACATCTCAAGTGACCCCGCAGCGC
GAGACGCGGGTGGCGGCAGGGCGTCCCAGGGTGCGGCACCGCGCTCCAGTCTTGGAAATA
ATTAGGCAAATCTAAAGGTCTCAAAGGAGCAAAGTAAACCGTGGAGGACAAAGAAAGGG
TTGTTATTTTGTCTTTCAGCCAGCCTGCTGGCTCCCAAGAGAGAGGCTTTTCAAGTTGAG
ACTCTGCTTAAGAGAAGATCAAAGTTAAAGCTCTGGGGTCAAGGGAGGGGCGGGGGCAGG
AAACTACCTCTGGCTTAATCTTTTAAAGCCAGTAGGAACCTTCTTAGGGATAGGTGGACC
CTGACATCCCTGTGGCTTGGCCAAAGGGCTCTGTGCTCTTCTGAGTCACAGTCTGGCAGGT
GATGGGGCTGGGGCCCCAGGCGTCAGCCTCCAGAGGGACAGCTGAGCCCCCTGCCTTGGC
TCCAGTTGGTGAAGCAGCCGAAGGGCTCTGACAGTGCCAGGGACCCCTGGGTCCCCA
GGCCTGCAGATGTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
ACCCCTGTGCCACCCAGAGCCCTGGGGGGTGGTCTCCATGCCGCCACCTGGCCTACCGCT
TTCTGTGCCGCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCTTGGGTTCTGTTTTT
TATAAACACCTCAAGCAGCACTGCAGTCTCCATCTCTCTGTTGGCTAAGCATACCCGCTT
CCAGCTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCCACTGCCCT
CATCCAGGCCTCTGACCAGTAGCTGAGAGGGGCTTTTTCTAGGCTTACAGCAGGGGAGAG
CTGGAAGGGGCTAGAAAGCTCCGCTTGTCTGTTTCTCAGGCTCTGTGAGCCTCAGTCTGT
AGACCAGATCAAGAGGAAGTACACGTCCCAATCACCCGTGTCAAGATTCACTCTCAGGAG
TGGGTGGCAGGAGAGGCAATAGCCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG
GTGTTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCAGACTCTGATCTCCAGGAACCCC
ATAGCCCTCTCCACTCCACCCCATGTTGATGCCAGGGTCACTCTTGTACCCGCTGGGCC
CCCAAACCCCGCTGCCTCTCTTCTTCCCCCATCCCCACCTGGTTTGTACTAATCTCTGC
TTCCCTCTCTGGGCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTAAAGAACTT
CTCGGGTGCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGAAGCAGAGCGCCACACTC
GCTGCTTAAGCTCCCCAGCTCTTTCAGAAAAACATAAATCAGAATTGTGTTTCAA

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41234
><subunit 1 of 1, 281 aa, 1 stop
><MW: 31743, pI: 6.83, NX(S/T): 1
MGRSGQQLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELSPFPDHAERAEQHEKYRP
SQDQGLPASRCLRCCDPGTSMPATAVPQINITILKGEKGRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMPGERCKSHYAAFVGRKKPMHSNHYQTVIDTEFVNLVDHFNMTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAI FSEELDTYITFSGYLVKHATEP

Signal sequence.

amino acids 1-25

N-glycosylation site.

amino acids 93-97

N-myristoylation sites.

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

Amidation site.

amino acids 150-154

Cell attachment sequence.

amino acids 104-107

FIGURE 31

GCGGAGCATCCGCTGCGGTCTCTGCGGAGACCCCGCGCGGATTGCGCGGTCTTCCCCGCGG
GCGGACAGAGCTGTCTTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGACGCCA
GAGAGAAATCTCATCATCTGTGCAGCCTTCTTAAAGCAAATAGACCTAGAGGGAGGAGTTAT
CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATGTTCTTCTCGGGGAGAGGGGAG
CTTGACTTACACTTTGGTAATAATTTGCTTCTGTACACTAAGGCTGTCTGTAGTCAGAATT
GCCTCAAAAAGAGTCTAGAAGATGTTGTCAATTGACATCCAGTCATCTCTTTCTAAGGGAATC
AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTCTGTCTTCAAC
AAAAAACATATCAGGGGACAAAGCATGTAACTTGATGATCTTCGACACTCGAAAAACAGCTA
GACAACCAACTGCTACCTATTTTCTGTCCCAACGAGGAAGCTGTCCATTGAAACAGCA
AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCAACAGCAGTCACTCCCC
TAGCCCATCATCACAGATTATTCAAAGCCCAACGATATCTCATGGAGAGACACTTTCT
CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
TAGCTCATCTGCTGCTGAAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA
CATACCACCTCGGCTACTCCAAGCCGCCACCCTTCTACCCACCAATGCTTCAAGTACACC
TTCTGGGACTTCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
AGCTTCCACGACCTCATTTCTACAGTTTTTACACGGGCTGCGGCTACACTCTCAAGCAATG
GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGACTCGAAAGGCAGCTTAGA
AACCATACCGTTTACAGAAATCTCCAACCTTAACTTTGAACACAGGGAATGTGTATAACCTA
CTGCACCTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAAGGT
AGGGAGGCCAGTCCAGGCAGTTCCTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCC
ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCCTGTTCTCTGGTGATAGGCC
TCGTCCTCTGGGTAGAATCTTTTCGGAATCACTCCGACAGGAACGTTACTCAAGACTGGAT
TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACTCGGTGTCTCTTAATTCATT
TAGTAACCAAGAACCCCAATGCAATGAGTTTCTGCTGACTTGCTAGCTTAGCAGGAGGTTG
TATTTTGAAGACAGGAAATGCCCCCTTCTGCTTTCCTTTTTTTTTTTGGAGACAGAGTCTT
GCTCTGTTGCCAGGCTGGAGTGCACTAGCAGATCTCGGCTCTCACGCAACCTCCGCTCTC
CTGGGTTCAAGCGATTCTCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
CCACACCTGGGTGATTTTGTATTTTAGTAGAGACGGGGTTTACCATTGTTGGTCAGGCTG
GTCTCAAACCTCTGACCTAGTGATCCACCCCTCTCGGCCCTCCAAAGTGCTGGGATTACAGG
CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTTGGTTTTTGAAGAAGGAATGAAGTG
GGAACCAAATAGGTAATTTGGGTAATCTGTCTCAAAATATAGCTAAAAACAAAGCTCT
ATGTAAGTAATAAAGTATAATTGCCATATAAAATTTCAAATTTCACTGGCTTTTATGCAAA
GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTTCTTGGTTCCAGATAAAATCAAC
TGTTTATATCAATTTCTAATGGATTGCTTTTCTTTTTATATGGATTCTTTAAAACTTATT
CCAGATGTAGTTCCTTCCAATTTAAATATTGAATAAATCTTTTGTACTCAA

FIGURE 32

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGLTYTLVIIICFLTRLLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASQQLLAYKEKGHSQSSQFSSDQEI AHL LPENV SALPATVAVASPH TTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEKWL LIGSLLFGVLFVLVIGLVLLGRILSESLRRKRYSLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 33

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGTCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCTCAAAGCTCCAGTCC
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTTCAGAGTGTCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGAAGTAAAGAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTGACGCAAAAGGCTTGAACCTCCCTTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTGAACACTGCAGGGTCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTGTAAACCAATGAACATTTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATTCCTTAAAAAAAAA

FIGURE 34

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777
><subunit 1 of 1, 235 aa, 1 stop
><MW: 25982, pI: 9.09, NX(S/T): 2
MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVVKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMEYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDAKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPIKERS
```

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125